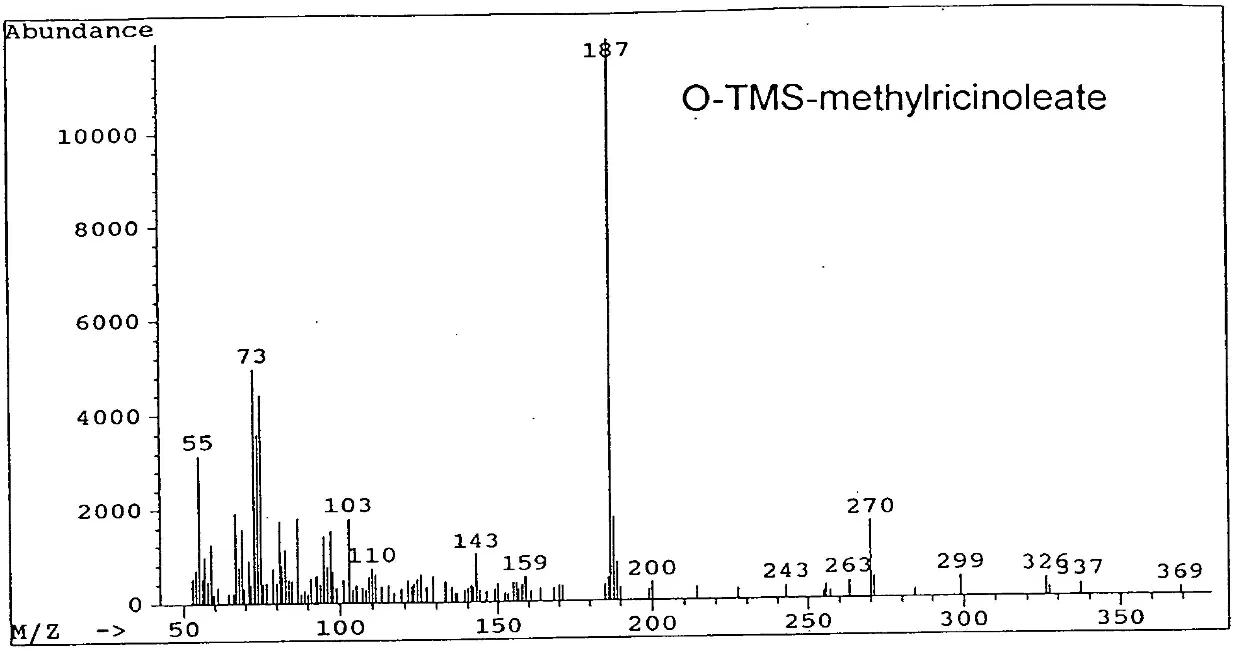
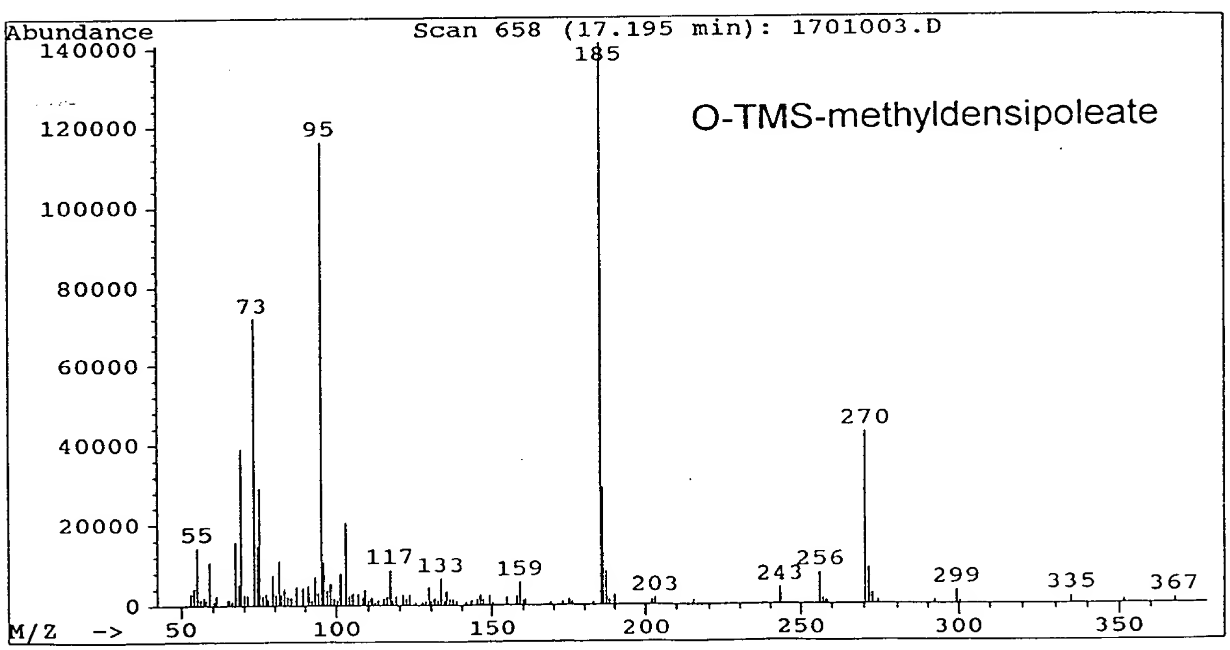
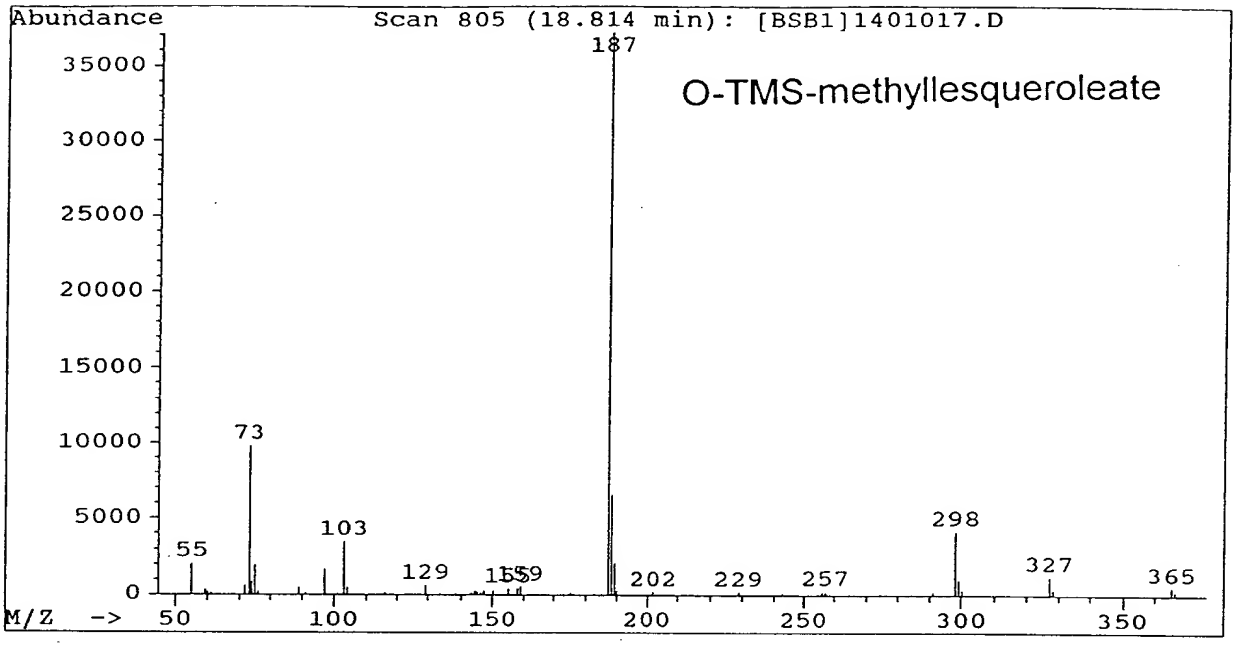
Figure 1A


Abundance
O-TMS-methylricinoleate
187
73
55
103
110
143
159
200
243
263
270
299
326
337
369
10000
8000
6000
4000
2000
0
M/Z ->
50
100
150
200
250
300
350

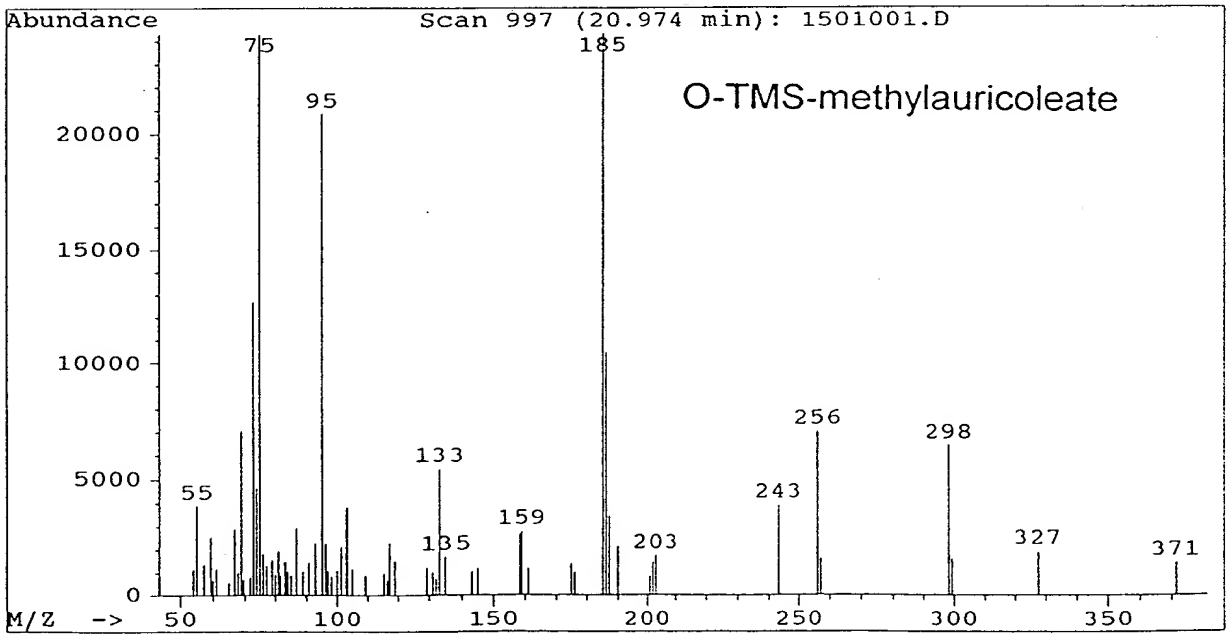
1B


Abundance
Scan 658 (17.195 min): 1701003.D
O-TMS-methyldensipoleate
185
95
73
55
117
133
159
203
243
256
270
299
335
367
140000
120000
100000
80000
60000
40000
20000
0
M/Z ->
50
100
150
200
250
300
350

1C

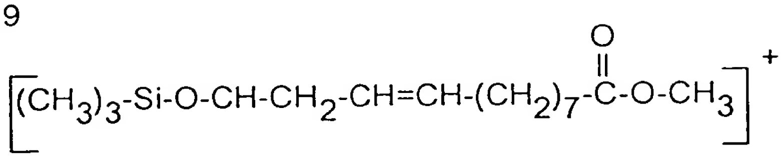

Abundance
Scan 805 (18.814 min): [BSB1]1401017.D
O-TMS-methyllesqueroleate
187
73
103
55
129
159
202
229
257
298
327
365
M/Z ->
50
100
150
200
250
300
350

1D

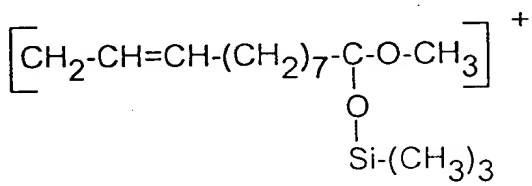

Abundance
Scan 997 (20.974 min): 1501001.D
O-TMS-methylauricoleate
75
185
95
133
256
298
55
243
159
135
203
327
371
M/Z ->
50
100
150
200
250
300
350

Ion #1: Mass 187 $[CH_3\text{-}(CH_2)_5\text{-}CH\text{-}O\text{-}Si\text{-}(CH_3)_3]^+$

Ion #2: Mass 299



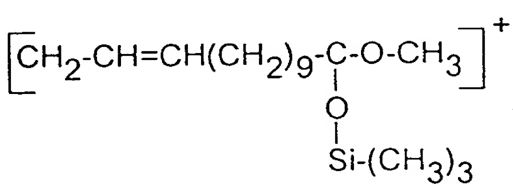
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)

$[CH_3\text{-}(CH_2)_2\text{-}CH{=}CH\text{-}CH_2\text{-}CH\text{-}O\text{-}Si\text{-}(CH_3)_3]^+$

Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of ion

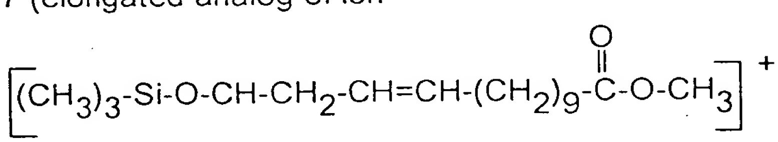


Figure 2

Figure 3

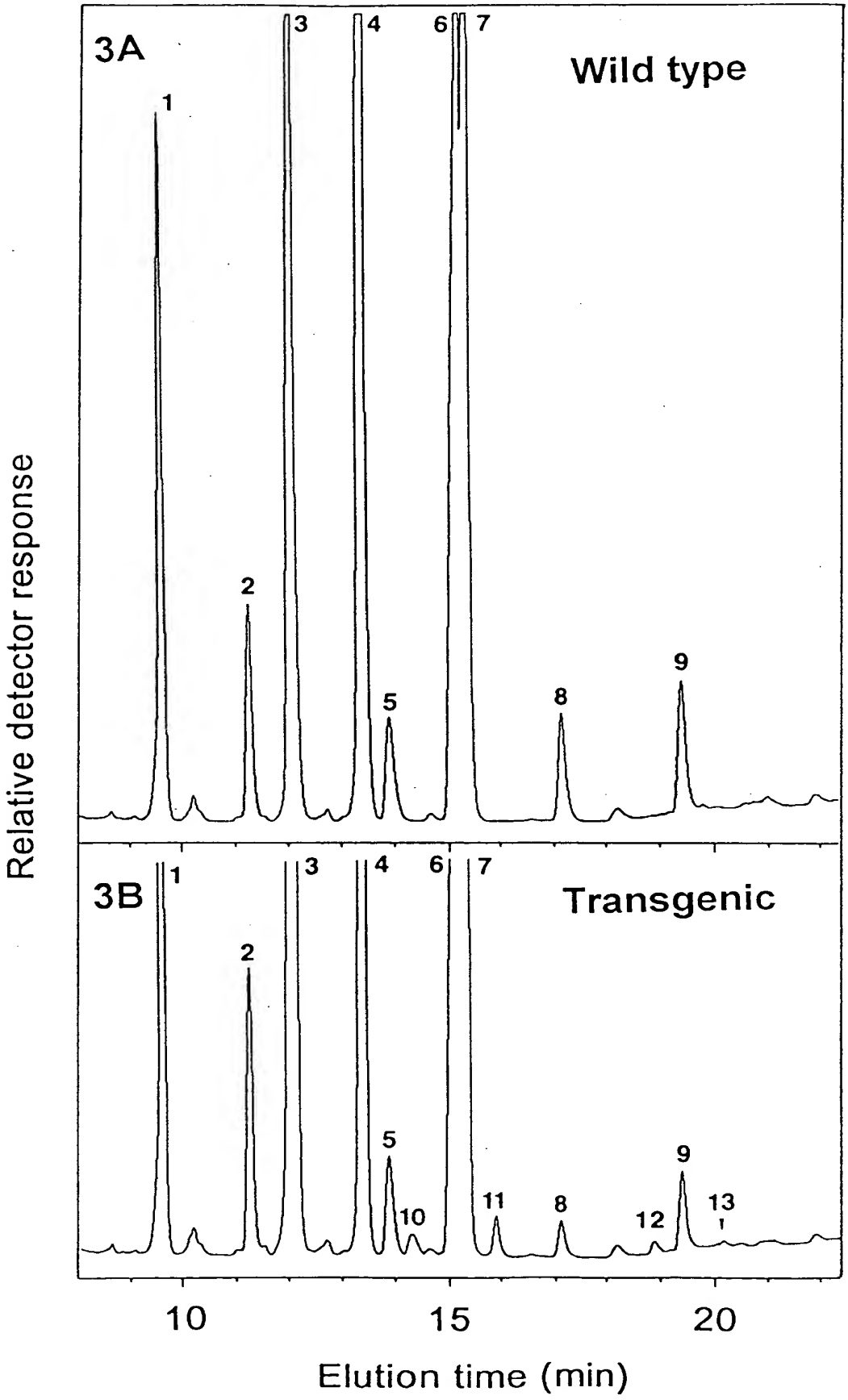
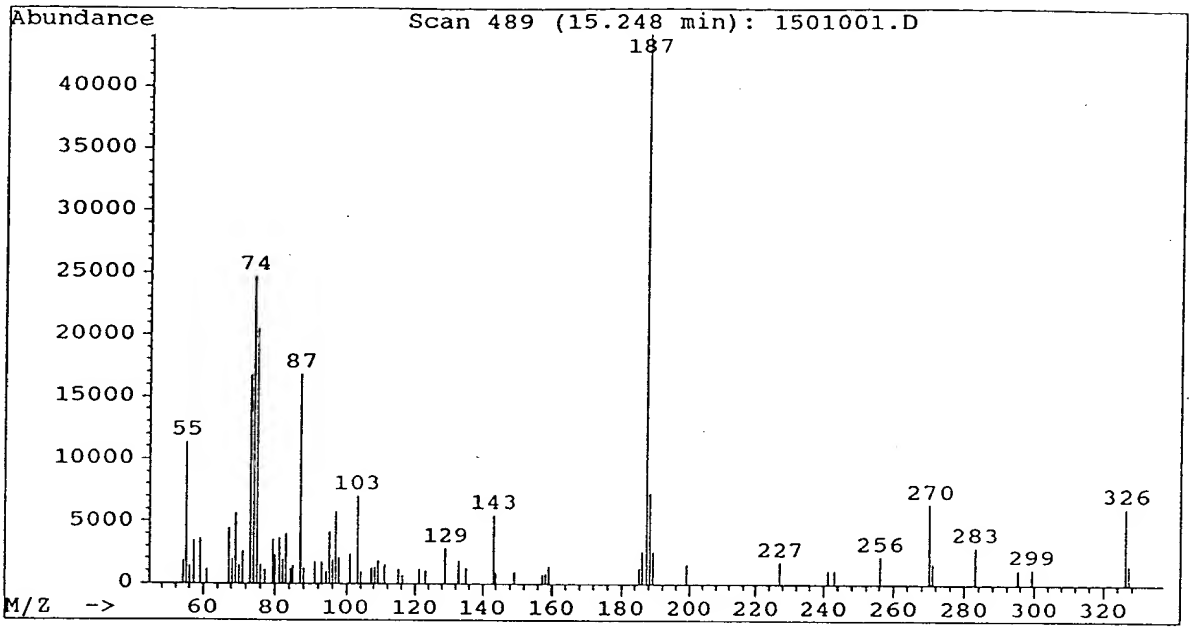
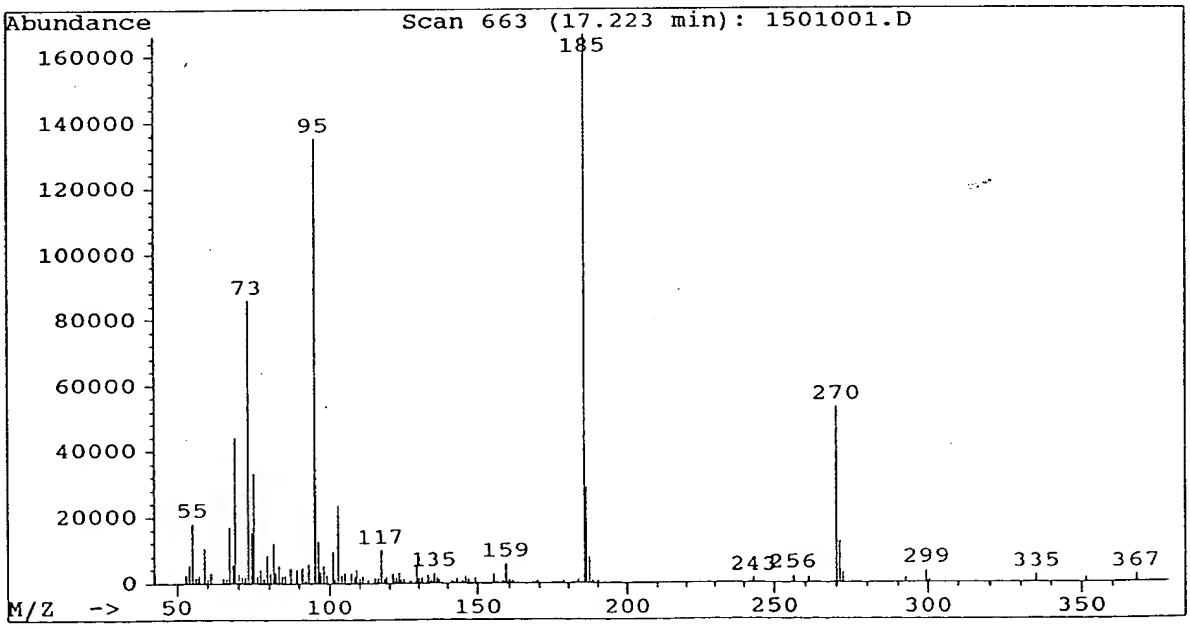

3A
Wild type
1
2
3
4
5
6
7
8
9
3B
Transgenic
1
2
3
4
5
6
7
8
9
10
11
12
13
Relative detector response
10
15
20
Elution time (min)

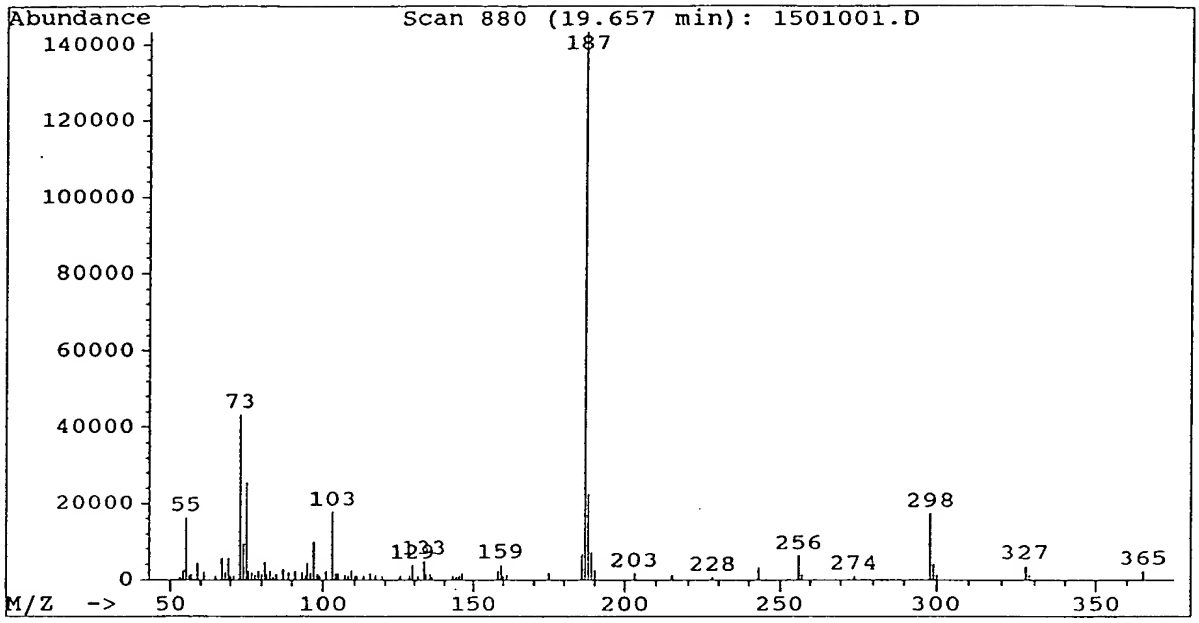
Figure 4A Mass spectrum of peak 10 from figure 3B



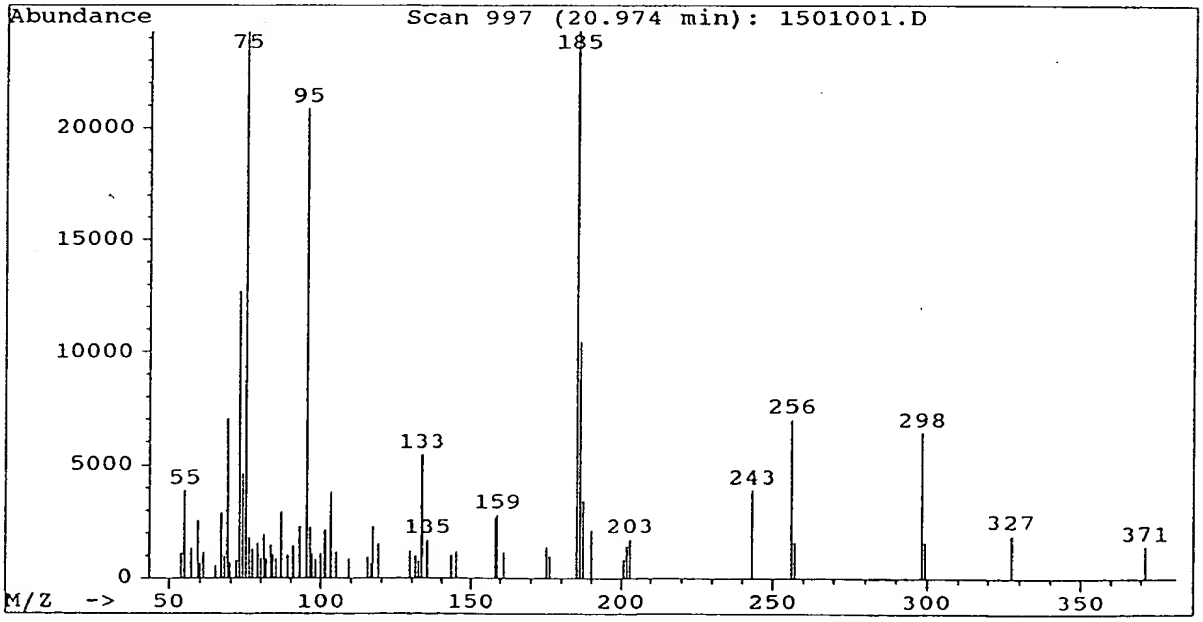
4B Mass spectrum of peak 11 from figure 3B



4C Mass spectrum of peak 12 from figure 3B



4D Mass spectrum of peak 13 from figure 3B



```
        10          20          30          40          50          60
TATTGGCACC  GGCGGCACCA  TTCCAACAAT  GGATCCCTAG  AAAAAGATGA  AGTCTTTGTC
        70          80          90         100         110         120
CCACCTAAGA  AAGCTGCAGT  CANATGGTAT  GTCAAATACC  TCAACAACCC  TCTTGGACGC
       130         140         150         160         170         180
ATTCTGGTGT  TAACAGTTCA  GTTTATCCTC  GGGTGGCCTT  TGTATCTAGC  CTTTAATGTA
       190         200         210         220         230         240
TCAGGTAGAC  CTTATGATGG  TTTCGCTTCA  CATTTCTTCC  CTCATGCACC  TATCTTTAAG
       250         260         270         280         290         300
GACCGTGAAC  GTCTCCAGAT  ATACATCTCA  GATGCTGGTA  TTCTAGCTGT  CTGTTATGGT
       310         320         330         340         350         360
CTTTACCGTT  ACGCTGCTTC  ACAAGGATTG  ACTGCTATGA  TCTGCGTCTA  CGGAGTACCG
       370         380         390         400         410         420
CTTTTGATAG  TGAACTTTTT  CCTTGTCTTG  GTCACTTTCT  TGCAGCACAC  TCATCCTTCA
       430         440         450         460         470         480
TTACCTCACT  ATGATTCAAC  CGAGTGGGAA  TGGATTAGAG  GAGCTTTGGT  TACGGTAGAC
       490         500         510         520         530         540
AGAGACTATG  GAATCTTGAA  CAAGGTGTTT  CACAACATAA  CAGACACCCA  CGTAGCACAC
       550
CAC
```

Figure 5

10	20	30	40	50	60
TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	AAAGAGATGA	AGTATTTGTC
70	80	90	100	110	120
CCAAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATGT	TAACTGTCCA	GTTCGTCCTC	GGATGGCCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAAC
250	260	270	280	290	300
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTTT	CCTCGTCTTG	ATCACTTACT	TACAACACAC	TCACCCTGCG
430	440	450	460	470	480
TTGCCTCACT	ATGATTCATC	AGAGTGGGAT	TGGCTTAGAG	GAGCTTTAGC	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTC	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					
CACT					

Figure 6

Figure 7

```
AT GAA GCT TTA TAA GAA GTT AGT TTT CTC TGG TGA CAG AGA AAT TNT      47

GTC AAT TGG TAG TGA CAG TTG AAG CAA CAG GAA CAA CAA GGA TGG TTG      95

GTG NTG ATG CTG ATG TGG TGA TGT GTT ATT CAT CAA ATA CTA AAT ACT     143

ACA TTA CTT GTT GCT GCC TAC TTC TCC TAT TTC CTC CGC CAC CCA TTT     191

TGG ACC CAC GAN CCT TCC ATT TAA ACC CTC TCT CGT GCT ATT CAC CAG     239

AAG AGA AGC CAA GAG AGA GAG AGA GAG AAT GTT CTG AGG ATC ATT GTC     287

TTC TTC ATC GTT ATT AAC GTA AGT TTT TTT TGA CCA CTC ATA TCT AAA     335

ATC TAG TAC ATG CAA TAG ATT AAT GAC TGT TCC TTC TTT TGA TAT TTT     383

                        Met Gly Ala Gly Gly Arg Ile Met Val Thr      10
CAG CTT CTT GAA TTC AAG ATG GGT GCT GGT GGA AGA ATA ATG GTT ACC     431

Pro Ser Ser Lys Lys Ser Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys      26
CCC TCT TCC AAG AAA TCA GAA ACT GAA GCC CTA AAA CGT GGA CCA TGT     479

Glu Lys Pro Pro Phe Thr Val Lys Asp Leu Lys Lys Ala Ile Pro Gln      42
GAG AAA CCA CCA TTC ACT GTT AAA GAT CTG AAG AAA GCA ATC CCA CAG     527

His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr      58
CAT TGT TTC AAG CGC TCT ATC CCT CGT TCT TTC TCC TAC CTT CTC ACA     575

Asp Ile Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe      74
GAT ATC ACT TTA GTT TCT TGC TTC TAC TAC GTT GCC ACA AAT TAC TTC     623

Ser Leu Leu Pro Gln Pro Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr      90
TCT CTT CTT CCT CAG CCT CTC TCT ACT TAC CTA GCT TGG CCT CTC TAT     671

Trp Val Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile Gly His     106
TGG GTA TGT CAA GGC TGT GTC TTA ACC GGT ATC TGG GTC ATT GGC CAT     719

Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr     122
GAA TGT GGT CAC CAT GCA TTC AGT GAC TAT CAA TGG GTA GAT GAC ACT     767

Val Gly Phe Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp     138
GTT GGT TTT ATC TTC CAT TCC TTC CTT CTC GTC CCT TAC TTC TCC TGG     815

Lys Tyr Ser His Arg Arg His His Ser Asn Asn Gly Ser Leu Glu Lys     154
AAA TAC AGT CAT CGT CGT CAC CAT TCC AAC AAT GGA TCT CTC GAG AAA     863

Asp Glu Val Phe Val Pro Pro Lys Lys Ala Ala Val Lys Trp Tyr Val     170
GAT GAA GTC TTT GTC CCA CCG AAG AAA GCT GCA GTC AAA TGG TAT GTT     911

Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Leu Val Leu Thr Val Gln     186
AAA TAC CTC AAC AAC CCT CTT GGA CGC ATT CTG GTG TTA ACA GTT CAG     959
```

Figure 8A

Phe Ile Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg 202
TTT ATC CTC GGG TGG CCT TTG TAT CTA GCC TTT AAT GTA TCA GGT AGA 1007

Pro Tyr Asp Gly Phe Ala Ser His Phe Phe Pro His Ala Pro Ile Phe 218
CCT TAT GAT GGT TTC GCT TCA CAT TTC TTC CCT CAT GCA CCT ATC TTT 1055

Lys Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu 234
AAA GAC CGA GAA CGC CTC CAG ATA TAC ATC TCA GAT GCT GGT ATT CTA 1103

Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr 250
GCT GTC TGT TAT GGT CTT TAC CGT TAC GCT GCT TCA CAA GGA TTG ACT 1151

Ala Met Ile Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Phe Phe 266
GCT ATG ATC TGC GTC TAT GGA GTA CCG CTT TTG ATA GTG AAC TTT TTC 1199

Leu Val Leu Val Thr Phe Leu Gln His Thr His Pro Ser Leu Pro His 282
CTT GTC TTG GTA ACT TTC TTG CAG CAC ACT CAT CCT TCG TTA CCT CAT 1247

Tyr Asp Ser Thr Glu Trp Glu Trp Ile Arg Gly Ala Leu Val Thr Val 298
TAT GAT TCA ACC GAG TGG GAA TGG ATT AGA GGA GCT TTG GTT ACG GTA 1295

Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp 314
GAC AGA GAC TAT GGA ATA TTG AAC AAG GTG TTC CAT AAC ATA ACA GAC 1343

Thr His Val Ala His His Leu Phe Ala Thr Ile Pro His Tyr Asn Ala 330
ACA CAT GTG GCT CAT CAT CTC TTT GCA ACT ATA CCG CAT TAT AAC GCA 1391

Met Glu Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His 346
ATG GAA GCT ACA GAG GCG ATA AAG CCA ATA CTT GGT GAT TAC TAC CAC 1439

Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu 362
TTC GAT GGA ACA CCG TGG TAT GTG GCC ATG TAT AGG GAA GCA AAG GAG 1487

Cys Leu Tyr Val Glu Pro Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr 378
TGT CTC TAT GTA GAA CCG GAT ACG GAA CGT GGG AAG AAA GGT GTC TAC 1535

Tyr Tyr Asn Asn Lys Leu 384
TAT TAC AAC AAT AAG TTA TGA GGC TGA TAG GGC GAG AGA AGT GCA ATT 1583

ATC AAT CTT CAT TTC CAT GTT TTA GGT GTC TTG TTT AAG AAG CTA TGC 1631

TTT GTT TCA ATA ATC TCA GAG TCC ATN TAG TTG TGT TCT GGT GCA TTT 1679

TGC CTA GTT ATG TGG TGT CGG AAG TTA GTG TTC AAA CTG CTT CCT GCT 1727

GTG CTG CCC AGT GAA GAA CAA GTT TAC GTG TTT AAA ATA CTC GGA ACG 1775

AAT TGA CCA CAA NAT ATC CAA AAC CGG CTA TCC GAA TTC CAT ATC CGA 1823

AAA CCG GAT ATC CAA ATT TCC AGA GTA CTT AG 1855

Figure 8B

```
                    10         20         30         40         50
LFFAH12      1 MGAGGRIM-- --VTPSSKKS --ETEALKRG PCEKPPFTVK DLKKAIPQHC      50
FAH12        1 MGGGGRMSTV ITSNNSEKKG --GSSHLKRA PHTKPPFTLG DLKRAIPPHC      50
ATFAD2       1 MGAGGRMP-- --VPTSSKKS --ETDTTKRV PCEKPPFSVG DLKKAIPPHC      50
BNFAD2       1 MGAGGRMQ-- --VSPPSKKS --ETDNIKRV PCETPPFTVG ELKKAIPPHC      50
GMFAD2-1     1 MGLA-KETTM GGRGRVAKVE VQGKKPLSRV PNTKPPFTVG QLKKAIPPHC      50
GMFAD2-2     1 MGAGGR---- TDVPPANRKS --EVDPLKRV PFEKPQFSLS QIKKAIPPHC      50
ZMFAD2       1 MGAGGRMTEK EREKQEQLAR ATGGAAMQRS PVEKPPFTLG QIKKAIPPHC      50
RCFAD2       1 ---------- ---------- ---------- ---------- ----------      50
                    60         70         80         90        100
LFFAH12     51 FKRSIPRSFS YLLTDITLVS CFYYVATNYF SLLPQPLSTY LAWPLYWVCQ     100
FAH12       51 FERSFVRSFS YVAYDVCLSF LFYSIATNFF PYISSPLS-Y VAWLVYWLFQ     100
ATFAD2      51 FKRSIPRSFS YLISDIIIAS CFYYVATNYF SLLPQPLS-Y LAWPLYWACQ     100
BNFAD2      51 FKRSIPRSFS HLIWDIIIAS CFYYVATTYF PLLPNPLS-Y FAWPLYWACQ     100
GMFAD2-1    51 FQRSLLTSFS YVVYDLSFAF IFY-IATTYF HLLPQPFS-L IAWPIYWVLQ     100
GMFAD2-2    51 FQRSVLRSFS YVVYDLTIAF CLYYVATHYF HLLPGPLS-F RGMAIYWAVQ     100
ZMFAD2      51 FERSVLKSFS YVVHDLVIAA ALLYFALAII PALPSPLR-Y AAWPLYWIAQ     100
RCFAD2      51 ---------- ---------- ---------- ---------- ----------     100
                   110        120        130        140        150
LFFAH12    101 GCVLTGIWVI GHECGHHAFS DYQWVDDTVG FIFHSFLLVP YFSWKYSHRR     150
FAH12      101 GCILTGLWVI GHECGHHAFS EYQLADDIVG LIVHSALLVP YFSWKYSHRR     150
ATFAD2     101 GCVLTGIWVI AHECGHHAFS DYQWLDDTVG LIFHSFLLVP YFSWKYSHRR     150
BNFAD2     101 GCVLTGVWVI AHECGHAAFS DYQWLDDTVG LIFHSFLLVP YFSWKYSHRR     150
GMFAD2-1   101 GCLLTGVWVI AHECGHHAFS KYQWVDDVVG LTLHSTLLVP YFSWKISHRR     150
GMFAD2-2   101 GCILTGVWVI AHECGHHAFS DYQLLDDIVG LILHSALLVP YFSWKYSHRR     150
ZMFAD2     101 G--------- -------AFS DYSLLDDVVG LVLHSSLMVP YFSWKYSHRR     150
RCFAD2     101 -------WVM AHDCGHHAFS DYQLLDDVVG LILHSCLLVP YFSWKHSHRR     150
                   160        170        180        190        200
LFFAH12    151 HHSNNGSLEK DEVFVPPKKA AVKWYVKYL- NNPLGRILVL TVQFILGWPL     200
FAH12      151 HHSNIGSLER DEVFVPKSKS KISWYSKYS- NNPPGRVLTL AATLLLGWPL     200
ATFAD2     151 HHSNTGSLER DEVFVPKQKS AIKWYGKYL- NNPLGRIMML TVQFVLGWPL     200
BNFAD2     151 HHSNTGSLER DEVFVPR-RS QTSSGTAST- STTFGRTVML TVQFTLGWPL     200
GMFAD2-1   151 HHSNTGSLDR DEVFVPKPKS KVAWFSKYL- NNPLGRAVSL LVTLTIGWPM     200
GMFAD2-2   151 HHSNTGSLER DEVFVPKQKS CIKWYSKYL- NNPPGRVLTL AVTLTLGWPL     200
ZMFAD2     151 HHSNTGSLER DEVFVPKKKE ALPWYTPYVY NNPVGRVVHI VVQLTLGWPL     200
RCFAD2     151 HHSNTGSLER DEVFVPKKKS SIRWYSKYL- NNPPGRIMTI AVTLSLGWPL     200
                   210        220        230        240        250
LFFAH12    201 YLAFNVSGRP YDG-FASHFF PHAPIFKDRE RLQIYISDAG ILAVCYGLYR     250
FAH12      201 YLAFNVSGRP YDR-FACHYD PYGPIFSERE RLQIYIADLG IFATTFVLYQ     250
ATFAD2     201 YLAFNVSGRP YDG-FACHFF PNAPIYNDRE RLQIYLSDAG ILAVCFGLYR     250
BNFAD2     201 YLAFNVSGRP YDGGFACHFH PNAPIYNDRE RLQIYISDAG ILAVCYGLLP     250
GMFAD2-1   201 YLAFNVSGRP YDS-FASHYH PYAPIYSNRE RLLIYVSDVA LFSVTYSLYR     250
GMFAD2-2   201 YLALNVSGRP YDR-FACHYD PYGPIYSDRE RLQIYISDAG VLAVVYGLFR     250
ZMFAD2     201 YLATNASGRP YPR-FACHFD PYGPIYNDRE RAQIFVSDAG VVAVAFGLYK     250
RCFAD2     201 YLAFNVSGRP YDR-FACHYD PYGPIYNDRE RIEIFISDAG VLAVTFGLYQ     250
```

Figure 9A

		260	270	280	290	300	
LFFAH12	251	YAASQGLTAM	ICVYGVPLLI	VNFFLVLVTF	LQHTHPSLPH	YDSTEWEWIR	300
FAH12	251	ATMAKGLAWV	MRIYGVPLLI	VNCFLVMITY	LQHTHPAIPR	YGSSEWDWLR	300
ATFAD2	251	YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
BNFAD2	251	YAAVQGVASM	VCFLRVPLLI	VNGFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
GMFAD2-1	251	VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTHFALPH	YDSSEWDWLK	300
GMFAD2-2	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITF	LQHTHPALPH	YTSSEWDWLR	300
ZMFAD2	251	LAAAFGVWWV	VRVYAVPLLI	VNAWLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
RCFAD2	251	LAIAKGLAWV	VCVYGVPLLV	VNSFLVLITF	LQHTHPALPH	YDSSEWDWLR	300

		310	320	330	340	350	
LFFAH12	301	GALVTVDRDY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG	350
FAH12	301	GAMVTVDRDY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYHAME	ATKAIKPIMG	350
ATFAD2	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
BNFAD2	301	GALATVDRDY	GILNQGFHNI	TDTHEAHHLF	STMPHYHAME	ATKAIKPILG	350
GMFAD2-1	301	GALATMDRDY	GILNKVFHHI	TDTHVAHHLF	STMPHYHAME	ATNAIKPILG	350
GMFAD2-2	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIKPILG	350
ZMFAD2	301	GALATMDRDY	GILNRVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIRPILG	350
RCFAD2	301	GALATVDRDY	GILNKVFHNI	TDTQVAHHLF	----------	----------	350
		360	370	380	390	400	
LFFAH12	351	DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVYYYNN	K-L.....	400
FAH12	351	EYYRYDGTPF	YKALWREAKE	CLFVEPDEGA	PTQGVFWYRN	KY-.....	400
ATFAD2	351	DYYQFDGTPW	YVAMYREAKE	CIYVEPDREG	DKKGVYWYNN	K-L.....	400
BNFAD2	351	EYYQFDGTPV	VKAMWREAKE	CIYVEPDRQG	EKKGVFWYNN	KL*.....	400
GMFAD2-1	351	EYYQFDDTPF	YKALWREARE	CLYVEPDEGT	SEKGVYWYRN	KY-.....	400
GMFAD2-2	351	EYYRFDETPF	VKAMWREARE	CIYVEPDQST	ESKGVFWYNN	KL-.....	400
ZMFAD2	351	DYYHFDPTPV	AKATWREAGE	CIYVEPE---	DRKGVFWYNK	KF*.....	400

Figure 9B

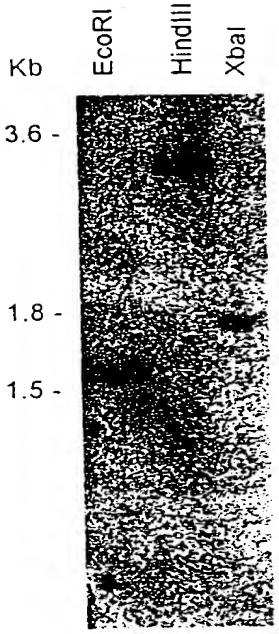
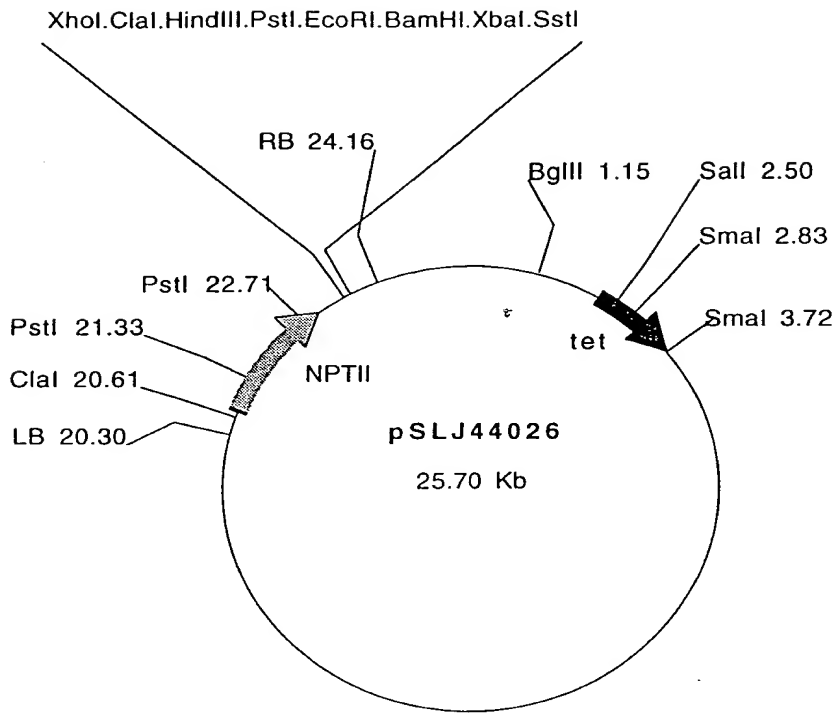


Figure 10



Plasmid name: pSLJ44026
Plasmid size: 25.70 kb
Constructed by: Jonathon Jones
Construction date: 1992
Comments/References: Transgenic Research 1,285-297 (1992)

Figure 11

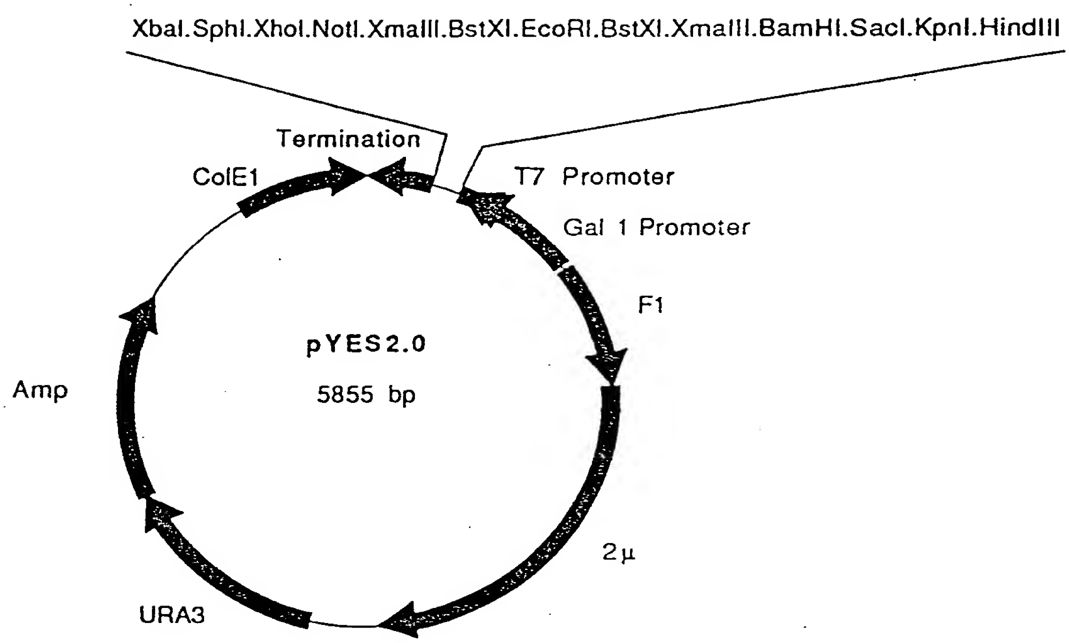

Xbal.Sphl.Xhol.Notl.XmaIII.BstXI.EcoRI.BstXI.XmaIII.BamHI.SacI.KpnI.HindIII
Termination
ColE1
T7 Promoter
Gal 1 Promoter
F1
pYES2.0
5855 bp
Amp
2μ
URA3

Figure 12

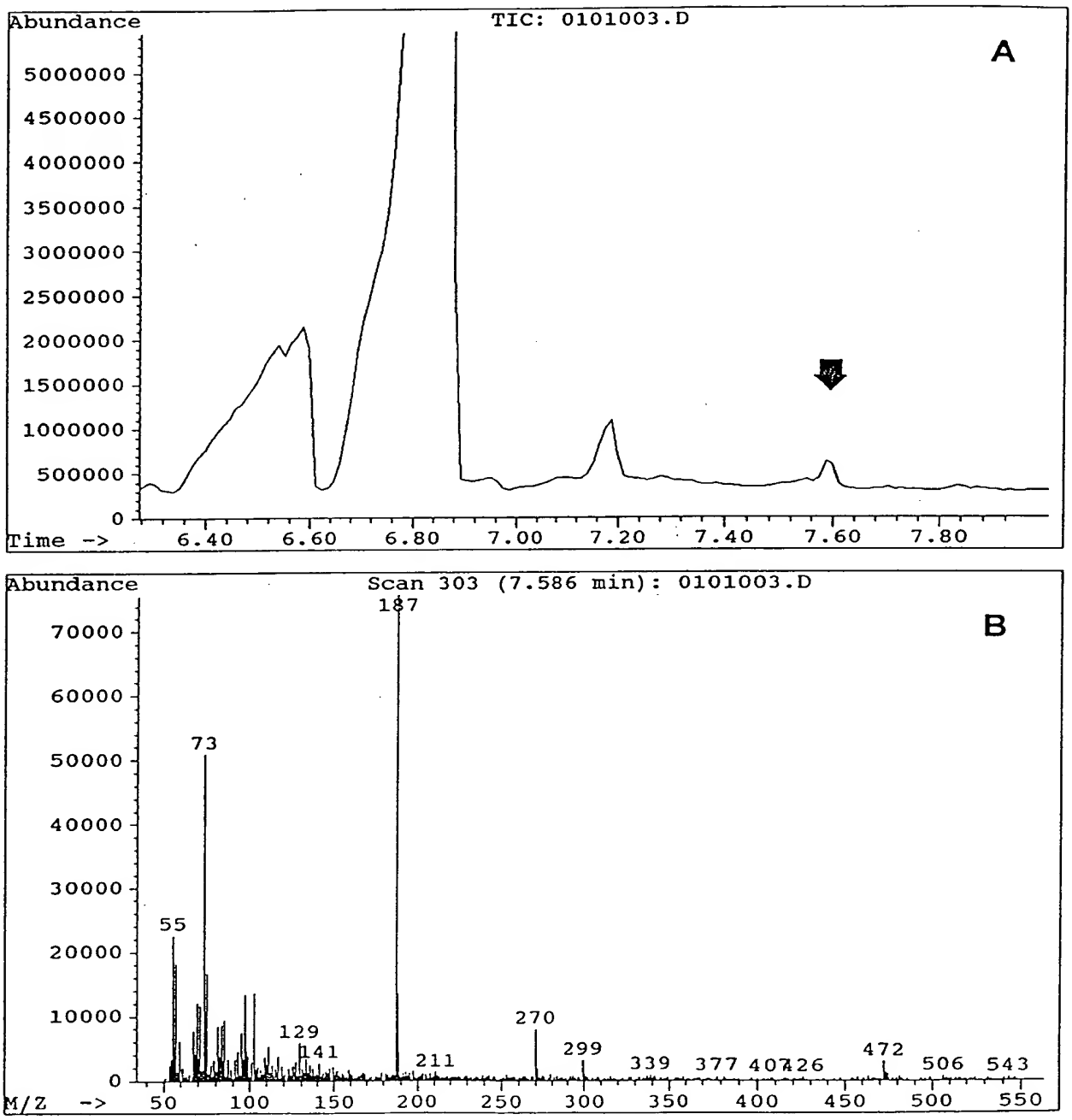

Abundance
TIC: 0101003.D
A
5000000
4500000
4000000
3500000
3000000
2500000
2000000
1500000
1000000
500000
0
Time ->
6.40
6.60
6.80
7.00
7.20
7.40
7.60
7.80
Abundance
Scan 303 (7.586 min): 0101003.D
B
187
73
55
129
141
211
270
299
339
377
407
426
472
506
543
70000
60000
50000
40000
30000
20000
10000
0
M/Z ->
50
100
150
200
250
300
350
400
450
500
550

Figure 13